

## Amendments to the Claims

This listing of claims will replace all prior versions and listings of all claims in the application.

Claims 1-27 (Cancelled)

28. (Withdrawn – Currently Amended) A method of screening for protozymes, said method comprising:

- a) identifying a suitable protein scaffold lacking a desirable enzyme-like activity
- b) inputting a protein backbone structure of said protein scaffold into a computer, wherein said backbone structure has variable residue positions;
- c) inserting an active site domain into said scaffold comprising the use of one or more high energy state rotamers;
- d) applying at least one protein design automation algorithm using the high energy rotamers comprising:
  - i) establishing a group of variable position rotamers for each of said variable positions;
  - ii) analyzing the interaction of each said high energy rotamers with said variable position rotamers; and
  - iii) analyzing the interaction of each said high energy rotamers with the remainder of said protein backbone;
- e) generating a set of candidate variant proteins with putative enzyme-like activity;
- f) synthesizing a plurality of said candidate variant proteins with putative enzyme-like activity; and,
- g) testing said candidate variant proteins with putative enzyme-like activity and selecting at least one of said candidate variant proteins with enzyme-like activity.

29. (Withdrawn) A method according to claim 28 wherein said insertion step is done at the same time as applying said protein design automation algorithm.

30. (Withdrawn) A method according to claim 28 further comprising applying a second protein design automation algorithm prior to said generating step.

31. (Withdrawn) A method according to claim 28 wherein said active site domain catalyzes a known enzymatic reaction.

32. (Withdrawn) A method according to claim 28 wherein said protein design automation algorithm comprises a DEE computation

33. (Withdrawn) A method according to claim 28 wherein said protein design cycle includes the use of at least one scoring function.

34. (Withdrawn) A method according to claim 33 wherein said scoring function is selected from the group consisting of a van der Waals potential scoring function, a hydrogen bond potential scoring function, an atomic solvation scoring function, an electrostatic scoring function and a secondary structure propensity scoring function.

35. (Withdrawn) A method according to claim 28 wherein said synthesizing includes a shuffling step.

36. (Withdrawn) A method according to claim 28 wherein said protein design algorithm comprises a force field calculation.

37. (New) A method of screening for protozymes, said method comprising:

- identifying a suitable protein scaffold lacking a desirable enzyme-like activity;
- inputting a protein backbone structure of said protein scaffold into a computer, wherein said backbone structure has variable residue positions ;
- inserting an active site domain into said scaffold comprising the use of one or more high energy state rotamers;
- applying at least one protein design cycle; and

- e) generating a set of candidate variant proteins with putative enzyme-like activity;
- f) synthesizing a plurality of said candidate variant proteins with putative enzyme-like activity; and,
- g) testing said candidate variant proteins with putative enzyme-like activity and selecting at least one of said candidate variant proteins with enzyme-like activity.

38. (New) A method according to claim 37 wherein said insertion step is done at the same time as applying said protein design automation algorithm.

39. (New) A method according to claim 37 further comprising applying a second protein design automation algorithm prior to said generating step.

40. (New) A method according to claim 37 wherein said active site domain catalyzes a known enzymatic reaction.

41. (New) A method according to claim 37 wherein said protein design automation algorithm comprises a DEE computation

42. (New) A method according to claim 37 wherein said protein design cycle includes the use of at least one scoring function.

43. (New) A method according to claim 42 wherein said scoring function is selected from the group consisting of a van der Waals potential scoring function, a hydrogen bond potential scoring function, an atomic solvation scoring function, an electrostatic scoring function and a secondary structure propensity scoring function.

44. (New) A method according to claim 37 wherein said synthesizing includes a shuffling step.

45. (New) A method according to claim 37 wherein said protein design algorithm comprises a force field calculation.